

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/033,662DATE: 08/08/98
TIME: 15:52:36

INPUT SET: S27966.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

ENTERED

1
2
3 (1) General Information:
4
5 (i) APPLICANT: HU, JING-SHAN
6 OLSEN, HENRIK S.
7 ROSEN, CRAIG A.
8
9 (ii) TITLE OF INVENTION: HUMAN VASCULAR ENDOTHELIAL GROWTH FACTOR 3
10
11 (iii) NUMBER OF SEQUENCES: 8
12
13 (iv) CORRESPONDENCE ADDRESS:
14 (A) ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
15 (B) STREET: 1100 NEW YORK AVE, NW
16 (C) CITY: WASHINGTON
17 (D) STATE: DC
18 (E) COUNTRY: USA
19 (F) ZIP: 20005
20
21 (v) COMPUTER READABLE FORM:
22 (A) MEDIUM TYPE: Floppy disk
23 (B) COMPUTER: IBM PC compatible
24 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
25 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
26
27 (vi) CURRENT APPLICATION DATA:
28 (A) APPLICATION NUMBER: US 09/033,662
29 (B) FILING DATE: 03-MAR-1998
30 (C) CLASSIFICATION:
31
32 (vii) PRIOR APPLICATION DATA:
33 (A) APPLICATION NUMBER: US 08/469,641
34 (B) FILING DATE: 06-JUN-1995
35
36 (viii) ATTORNEY/AGENT INFORMATION:
37 (A) NAME: STEFFE, ERIC K.
38 (B) REGISTRATION NUMBER: 36,688
39 (C) REFERENCE/DOCKET NUMBER: 1488.1040001
40
41 (ix) TELECOMMUNICATION INFORMATION:
42 (A) TELEPHONE: 202-371-2600
43 (B) TELEFAX: 202-371-2540
44
45
46 (2) INFORMATION FOR SEQ ID NO:1:

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47
48      (i) SEQUENCE CHARACTERISTICS:
49          (A) LENGTH: 666 base pairs
50          (B) TYPE: nucleic acid
51          (C) STRANDEDNESS: both
52          (D) TOPOLOGY: both
53
54      (ii) MOLECULE TYPE: cDNA
55
56
57      (ix) FEATURE:
58          (A) NAME/KEY: CDS
59          (B) LOCATION: 1..663
60
61
62      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
63
64      ATG AGA AGG TGT AGA ATA AGT GGG AGG CCC CCG GCG CCC CCC GGT GTC      48
65      Met Arg Arg Cys Arg Ile Ser Gly Arg Pro Pro Ala Pro Pro Gly Val
66          1              5              10              15
67
68      CCC GCC CAG GCC CCT GTC TCC CAG CCT GAT GCC CCT GGC CAC CAG AGG      96
69      Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His Gln Arg
70              20              25              30
71
72      AAA GTG GTG TCA TGG ATA GAT GTG TAT ACT CGC GCT ACC TGC CAG CCC      144
73      Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys Gln Pro
74          35              40              45
75
76      CGG GAG GTG GTG GTG CCC TTG ACT GTG GAG CTC ATG GGC ACC GTG GCC      192
77      Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr Val Ala
78          50              55              60
79
80      AAA CAG CTG GTG CCC AGC TGC GTG ACT GTG CAG CGC TGT GGT GGC TGC      240
81      Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly Cys
82          65              70              75              80
83
84      TGC CCT GAC GAT GGC CTG GAG TGT GTG CCC ACT GGG CAG CAC CAA GTC      288
85      Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln Val
86              85              90              95
87
88      CGG ATG CAG ATC CTC ATG ATC CGG TAC CCG AGC AGT CAG CTG GGG GAG      336
89      Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu Gly Glu
90              100              105              110
91
92      ATG TCC CTG GAA GAA CAC AGC CAG TGT GAA TGC AGA CCT AAA AAA AAG      384
93      Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys Lys Lys
94          115              120              125
95
96      GAC AGT GCT GTG AAG CCA GAC AGG GCT GCT ACT CCC CAC CAC CGT CCC      432
97      Asp Ser Ala Val Lys Pro Asp Arg Ala Ala Thr Pro His His Arg Pro
98          130              135              140
99
  
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100	CAG	CCC	CGT	TCT	GTT	CCG	GGC	TGG	GAC	TCT	GCC	CCC	GGA	GCA	CCC	TCC	480
101	Gln	Pro	Arg	Ser	Val	Pro	Gly	Trp	Asp	Ser	Ala	Pro	Gly	Ala	Pro	Ser	
102	145					150					155					160	
103																	
104	CCA	GCT	GAC	ATC	ACC	CAA	TCC	CAC	TCC	AGC	CCC	AGG	CCC	CTC	TGC	CCA	528
105	Pro	Ala	Asp	Ile	Thr	Gln	Ser	His	Ser	Ser	Pro	Arg	Pro	Leu	Cys	Pro	
106					165					170					175		
107																	
108	CGC	TGC	ACC	CAG	CAC	CAC	CAG	TGC	CCT	GAC	CCC	CGG	ACC	TGC	CGC	TGC	576
109	Arg	Cys	Thr	Gln	His	His	Gln	Cys	Pro	Asp	Pro	Arg	Thr	Cys	Arg	Cys	
110				180					185					190			
111																	
112	CGC	TGT	CGA	CGC	CGC	AGC	TTC	CTC	CGT	TGT	CAA	GGG	CGG	GGC	TTA	GAG	624
113	Arg	Cys	Arg	Arg	Arg	Ser	Phe	Leu	Arg	Cys	Gln	Gly	Arg	Gly	Leu	Glu	
114			195					200					205				
115																	
116	CTC	AAC	CCA	GAC	ACC	TGC	AGG	TGC	CGG	AAG	CTG	CGA	AGG	TGA			666
117	Leu	Asn	Pro	Asp	Thr	Cys	Arg	Cys	Arg	Lys	Leu	Arg	Arg				
118		210					215					220					
119																	
120																	
121	(2) INFORMATION FOR SEQ ID NO:2:																
122																	
123	(i) SEQUENCE CHARACTERISTICS:																
124	(A) LENGTH: 221 amino acids																
125	(B) TYPE: amino acid																
126	(D) TOPOLOGY: linear																
127																	
128	(ii) MOLECULE TYPE: protein																
129																	
130	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:																
131																	
132	Met	Arg	Arg	Cys	Arg	Ile	Ser	Gly	Arg	Pro	Pro	Ala	Pro	Pro	Gly	Val	
133	1				5					10					15		
134																	
135	Pro	Ala	Gln	Ala	Pro	Val	Ser	Gln	Pro	Asp	Ala	Pro	Gly	His	Gln	Arg	
136				20		</											

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153 Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys Lys Lys
154 115 120 125
155
156 Asp Ser Ala Val Lys Pro Asp Arg Ala Ala Thr Pro His His Arg Pro
157 130 135 140
158
159 Gln Pro Arg Ser Val Pro Gly Trp Asp Ser Ala Pro Gly Ala Pro Ser
160 145 150 155 160
161
162 Pro Ala Asp Ile Thr Gln Ser His Ser Ser Pro Arg Pro Leu Cys Pro
163 165 170 175
164
165 Arg Cys Thr Gln His His Gln Cys Pro Asp Pro Arg Thr Cys Arg Cys
166 180 185 190
167
168 Arg Cys Arg Arg Arg Ser Phe Leu Arg Cys Gln Gly Arg Gly Leu Glu
169 195 200 205
170
171 Leu Asn Pro Asp Thr Cys Arg Cys Arg Lys Leu Arg Arg
172 210 215 220
173
174

175 (2) INFORMATION FOR SEQ ID NO:3:

176 (i) SEQUENCE CHARACTERISTICS:

- 177 (A) LENGTH: 29 base pairs
178 (B) TYPE: nucleic acid
179 (C) STRANDEDNESS: both
180 (D) TOPOLOGY: linear
181
182

183 (ii) MOLECULE TYPE: cDNA

184

185

186

187

188 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

189

190 GCATGGATCC CAGCCTGATG CCCCTGGCC

29

191

192 (2) INFORMATION FOR SEQ ID NO:4:

193

194 (i) SEQUENCE CHARACTERISTICS:

- 195 (A) LENGTH: 30 base pairs
196 (B) TYPE: nucleic acid
197 (C) STRANDEDNESS: both
198 (D) TOPOLOGY: linear
199

200 (ii) MOLECULE TYPE: cDNA

201

202

203

204

205 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

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206
207 GCATTCTAGA CCCTGCTGAG TCTGAAAAGC 30
208
209 (2) INFORMATION FOR SEQ ID NO:5:
210
211 (i) SEQUENCE CHARACTERISTICS:
212 (A) LENGTH: 29 base pairs
213 (B) TYPE: nucleic acid
214 (C) STRANDEDNESS: both
215 (D) TOPOLOGY: linear
216
217 (ii) MOLECULE TYPE: cDNA
218
219
220
221
222 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
223
224 GACTGCATGC ACCAGAGGAA AGTGGTGTG 29
225
226 (2) INFORMATION FOR SEQ ID NO:6:
227
228 (i) SEQUENCE CHARACTERISTICS:
229 (A) LENGTH: 29 base pairs
230 (B) TYPE: nucleic acid
231 (C) STRANDEDNESS: both
232 (D) TOPOLOGY: linear
233
234 (ii) MOLECULE TYPE: cDNA
235
236
237
238
239 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
240
241 GACTAGATCT CCTTCGCAGC TTCCGGCAC 29
242
243 (2) INFORMATION FOR SEQ ID NO:7:
244
245 (i) SEQUENCE CHARACTERISTICS:
246 (A) LENGTH: 14 amino acids
247 (B) TYPE: amino acid
248 (C) STRANDEDNESS: single
249 (D) TOPOLOGY: Not Relevant
250
251 (ii) MOLECULE TYPE: peptide
252
253
254
255
256 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:
257
258 Pro Xaa Cys Val Xaa Xaa Xaa Arg Cys Xaa Gly Cys Cys Asn

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SEQUENCE VERIFICATION REPORT
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Original Text